```
=> d his

        (FILE 'HOME' ENTERED AT 16:53:20 ON 22 DEC 2004)

        FILE 'MEDLINE' ENTERED AT 16:53:36 ON 22 DEC 2004
L1      100313 S SPECIFIC?(3A)ANTIBOD?
L2        1669 S HUMAN(1A)(CYTOKINE# OR (GROWTH ADJ FACTOR#) OR LYMPHOKINE#)
L3           0 S L1(3A)L2
L4           3 S L1(5A)L2


        FILE 'STNGUIDE' ENTERED AT 16:57:02 ON 22 DEC 2004

        FILE 'MEDLINE' ENTERED AT 17:18:01 ON 22 DEC 2004
L5        5952 S (CROSS-REACT? OR CROSSREACT?)(2A)ANTIBOD?
L6        1793 S L1 AND L5
L7        7377 S ANTI-HUMAN
L8          33 S L6 AND L7


        FILE 'STNGUIDE' ENTERED AT 17:20:37 ON 22 DEC 2004

        FILE 'MEDLINE' ENTERED AT 17:37:07 ON 22 DEC 2004
L9         240 S RESPONS?(1A)XENOG?
L10        455 S SPECIES-SPECIFIC(2A)ANTIBOD?
L11          1 S L9 AND L10
L12      22227 S (SCID OR NUDE)(W)(MICE OR MOUSE)
L13         29 S L9 AND L12
L14         14 S L10 AND L12


        FILE 'STNGUIDE' ENTERED AT 17:39:57 ON 22 DEC 2004

        FILE 'MEDLINE' ENTERED AT 17:46:10 ON 22 DEC 2004
L15         59 S (NONCROSS-REACT? OR NON-CROSS-REACT? OR NON-CROSSREACT?)(2A)A
L16          0 S L12 AND L15

        FILE 'STNGUIDE' ENTERED AT 17:49:20 ON 22 DEC 2004
```

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on:  November 1, 2004, 20:43:02 ; Search time 98.6988 Seconds
(without alignments)
890.474 Million cell updates/sec

Title:  US-10-017-910-2
Perfect score: 1299
Sequence: 1 QMDPNRISEDGTHCIYRILR..........LLDPDQDATYFGAPKVRDID 245

Scoring table:  BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters:  2002273

Post-processing: Minimum Match 0%
Maximum Match 100%
Minimum DB seq length: 0
Maximum DB seq length: 200000000

Database :  A_Geneseq_23Sep04:*
Listing first 45 summaries
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query Match | Match Length | DB | ID | Description |
| --- | --- | --- | --- | --- | --- | --- |
| 1 | 1299 | 100.0 | 245 | 2 | AAY17873 | Aay17873 Human TRA |
| 2 | 1299 | 100.0 | 245 | 6 | ABU08462 | Abu08462 Amino aci |
| 3 | 1293 | 99.5 | 249 | 5 | ABG94282 | Abg94282 Human RAN |
| 4 | 1293 | 99.5 | 249 | 5 | ABG80594 | Abg80594 Human rec |
| 5 | 1293 | 99.5 | 249 | 7 | ADJ82115 | Adj82115 Protein f |
| 6 | 1293 | 99.5 | 250 | 6 | ADA50079 | Ada50079 Human wil |
| 7 | 1293 | 99.5 | 270 | 4 | ADJ82113 | Adj82113 Protein f |
| 8 | 1293 | 99.5 | 317 | 2 | AAW83018 | Aaw83018 Osteoclas |
| 9 | 1293 | 99.5 | 317 | 2 | AAW83195 | Aaw83195 Human ost |
| 10 | 1293 | 99.5 | 317 | 2 | AAW69957 | Aaw69957 NF-kB rec |
| 11 | 1293 | 99.5 | 317 | 2 | AAW68293 | Aaw68293 NF-kB rec |
| 12 | 1293 | 99.5 | 317 | 2 | AAE08738 | Aae08738 Human rec |
| 13 | 1293 | 99.5 | 317 | 3 | AAX84417 | Aax84417 Amino aci |
| 14 | 1293 | 99.5 | 317 | 4 | AAE04426 | Aae04426 Human rec |
| 15 | 1293 | 99.5 | 317 | 4 | AAE01993 | Aae01993 Human ful |
| 16 | 1293 | 99.5 | 317 | 5 | ABB08134 | Abb08134 Human RAN |
| 17 | 1293 | 99.5 | 317 | 5 | AAE26103 | Aae26103 Human RAN |
| 18 | 1293 | 99.5 | 317 | 5 | ABG31631 | Abg31631 Human RAN |
| 19 | 1293 | 99.5 | 317 | 5 | AAU78285 | Aau78285 Human TRA |
| 20 | 1293 | 99.5 | 317 | 5 | AAO19096 | Aao19096 C neoform |
| 21 | 1293 | 99.5 | 317 | 6 | ABP55108 | Abp55108 Human ost |
| 22 | 1293 | 99.5 | 317 | 6 | AAE34364 | Aae34364 Human rec |
| 23 | 1293 | 99.5 | 317 | 6 | ABR42314 | Abr42314 Human RAN |
| 24 | 1293 | 99.5 | 317 | 7 | ADB16988 | Adb16988 Human rec |
| 25 | 1293 | 99.5 | 317 | 7 | ADC35204 | Adc35204 Human TNF |
| 26 | 1293 | 99.5 | 317 | 7 | ADC73002 | Adc73002 Human RAN |
| 27 | 1293 | 99.5 | 317 | 7 | ADC78268 | Adc78268 Human RAN |
| 28 | 1293 | 99.5 | 317 | 7 | ABW02277 | Abw02277 Human RAN |
| 29 | 1293 | 99.5 | 317 | 7 | ADG46723 | Adg46723 Human RAN |
| 30 | 1293 | 99.5 | 317 | 7 | ADJ82112 | Adj82112 Protein f |
| 31 | 1293 | 99.3 | 317 | 8 | ADM96241 | Adm96241 Human rec |
| 32 | 1290 | 99.3 | 250 | 6 | ADA50101 | Ada50101 Human RAN |
| 33 | 1290 | 99.3 | 250 | 6 | ADA50095 | Ada50095 Human RAN |
| 34 | 1290 | 99.3 | 250 | 6 | ADA50094 | Ada50094 Human RAN |
| 35 | 1290 | 99.3 | 250 | 6 | ADA50098 | Ada50098 Human RAN |
| 36 | 1289 | 99.3 | 250 | 6 | ADA50102 | Ada50102 Human RAN |
| 37 | 1289 | 99.2 | 250 | 6 | ADA50089 | Ada50089 Human RAN |
| 38 | 1289 | 99.2 | 250 | 6 | ADA50086 | Ada50086 Human RAN |
| 39 | 1289 | 99.2 | 250 | 6 | ADA50099 | Ada50099 Human RAN |
| 40 | 1288 | 99.2 | 244 | 5 | ABG94283 | Abg94283 Human RAN |
| 41 | 1288 | 99.2 | 244 | 5 | AAU86148 | Aau86148 Human PRO |
| 42 | 1288 | 99.2 | 244 | 5 | AAU78286 | Aau78286 Human TRA |
| 43 | 1288 | 99.2 | 244 | 5 | ABG80595 | Abg80595 Human rec |
| 44 | 1288 | 99.2 | 244 | 7 | ADC78865 | Adc78865 Human PRO |
| 45 | 1288 | 99.2 | 244 | 7 | ADJ37323 | Adj37323 Human tum |

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on:  November 1, 2004, 20:51:51 ; Search time 24.4563 Seconds
(without alignments)
664.364 Million cell updates/sec

Title:  US-10-017-910-2
Perfect score: 1299
Sequence: 1 QMDPNRISEDGTHCIYRILR..........LLDPDQDATYFGAPKVRDID 245

Scoring table:  BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters:  478139

Post-processing: Minimum Match 0%
Maximum Match 100%
Minimum DB seq length: 0
Maximum DB seq length: 200000000

Database :  Issued_Patents_AA:*
Listing first 45 summaries
1: /cgn2_6/ptcdata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptcdata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptcdata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptcdata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptcdata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptcdata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

*

OM protein - protein search, using sw model

Run on:        November 1, 2004, 20:54:17 ; Search time 73.8057 Seconds
                                            (without alignments)
                                            1076.243 Million cell updates/sec

Title:         US-10-017-910-2
Perfect score: 1299
Sequence:      1 QMDPNRISEDGTHCIYRILR.........LLDPDQDATYFGAPKVRDID 245

Scoring table: BLOSUM62
               Gapop 10.0 , Gapext 0.5

Searched:      1370721 seqs, 324215800 residues

Total number of hits satisfying chosen parameters:     1370721

Minimum DB seq length: 0

| Result No. | Score | Query % Match | Length | DB | ID | Description |
|---|---|---|---|---|---|---|
| 1 | 1293 | 99.5 | 317 | 3 | US-08-996-139-13 | Sequence 13, Appl |
| 2 | 1293 | 99.5 | 317 | 3 | US-08-995-659-13 | Sequence 13, Appl |
| 3 | 1293 | 99.5 | 317 | 3 | US-09-215-649A-13 | Sequence 13, Appl |
| 4 | 1293 | 99.5 | 317 | 4 | US-09-052-521C-4 | Sequence 4, Appli |
| 5 | 1293 | 99.5 | 317 | 13 | US-09-577-780-13 | Sequence 13, Appl |
| 6 | 1293 | 99.5 | 317 | 13 | US-09-577-800-13 | Sequence 13, Appl |
| 7 | 1293 | 99.5 | 317 | 13 | US-09-466-496-13 | Sequence 13, Appl |
| 8 | 1293 | 99.5 | 317 | 13 | US-09-871-856-13 | Sequence 13, Appl |
| 9 | 1293 | 99.5 | 317 | 13 | US-09-871-291-13 | Sequence 13, Appl |
| 10 | 1293 | 99.5 | 317 | 2 | US-09-396-937-2 | Sequence 2, Appli |
| 11 | 1293 | 99.5 | 317 | 13 | US-09-877-650-13 | Sequence 13, Appl |
| 12 | 1293 | 99.5 | 317 | 13 | US-09-865-363-13 | Sequence 13, Appl |
| 13 | 1108 | 85.3 | 294 | 3 | US-08-996-139-11 | Sequence 11, Appl |
| 14 | 1108 | 85.3 | 294 | 3 | US-08-995-659-11 | Sequence 11, Appl |
| 15 | 1108 | 85.3 | 294 | 3 | US-09-215-649A-11 | Sequence 11, Appl |
| 16 | 1108 | 85.3 | 294 | 4 | US-09-577-780-11 | Sequence 11, Appl |
| 17 | 1108 | 85.3 | 294 | 4 | US-09-577-800-11 | Sequence 11, Appl |
| 18 | 1108 | 85.3 | 294 | 4 | US-09-466-496-11 | Sequence 11, Appl |
| 19 | 1108 | 85.3 | 294 | 4 | US-09-871-856-11 | Sequence 11, Appl |
| 20 | 1108 | 85.3 | 294 | 4 | US-09-871-291-11 | Sequence 11, Appl |
| 21 | 1108 | 85.3 | 294 | 4 | US-09-877-650-11 | Sequence 11, Appl |
| 22 | 1108 | 85.3 | 294 | 2 | US-09-865-363-11 | Sequence 11, Appl |
| 23 | 1108 | 84.8 | 316 | 2 | US-08-842-842-7 | Sequence 7, Appli |
| 24 | 1108 | 84.8 | 316 | 2 | US-08-989-362-2 | Sequence 2, Appli |
| 25 | 1101 | 84.8 | 316 | 2 | US-09-052-521C-2 | Sequence 2, Appli |
| 26 | 1101 | 84.8 | 316 | 3 | US-09-671-658A-2 | Sequence 2, Appli |
| 27 | 1101 | 84.8 | 316 | 4 | US-09-396-937-6 | Sequence 6, Appli |
| 28 | 1101 | 84.8 | 316 | 4 | US-09-396-937-8 | Sequence 8, Appli |
| 29 | 767 | 59.0 | 187 | 4 | US-09-396-937-8 | Sequence 8, Appli |
| 30 | 767 | 58.9 | 173 | 4 | US-09-396-937-10 | Sequence 10, Appl |
| 31 | 755 | 58.1 | 173 | 4 | US-09-396-937-12 | Sequence 12, Appl |
| 32 | 717.5 | 55.2 | 188 | 3 | US-09-396-937-14 | Sequence 14, Appl |
| 33 | 707.5 | 54.5 | 182 | 4 | US-09-396-937-16 | Sequence 16, Appl |
| 34 | 687 | 52.9 | 173 | 4 | US-09-396-937-18 | Sequence 18, Appl |
| 35 | 666 | 51.3 | 173 | 4 | US-09-396-937-20 | Sequence 20, Appl |
| 36 | 414 | 31.9 | 77 | 4 | US-09-632-287A-11 | Sequence 11, Appl |
| 37 | 359 | 27.6 | 77 | 4 | US-09-632-287A-10 | Sequence 10, Appl |
| 38 | 235.5 | 18.1 | 253 | 3 | US-09-320-424-11 | Sequence 11, Appl |
| 39 | 235.5 | 18.1 | 253 | 3 | US-09-825-563-11 | Sequence 11, Appl |
| 40 | 235.5 | 18.1 | 256 | 3 | US-09-320-424-13 | Sequence 13, Appl |
| 41 | 235.5 | 18.1 | 256 | 4 | US-09-825-563-13 | Sequence 13, Appl |
| 42 | 234.5 | 18.1 | 279 | 3 | US-09-072-993C-3 | Sequence 3, Appli |
| 43 | 234.5 | 18.1 | 281 | 3 | US-08-670-354-2 | Sequence 2, Appli |
| 44 | 234.5 | 18.1 | 281 | 3 | US-08-584-031-1 | Sequence 1, Appli |
| 45 | 234.5 | 18.1 | 281 | 3 | US-08-780-496-1 | Sequence 1, Appli |

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Published_Applications_AA:*
  1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
  2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
  3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
  4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
  5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
  6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
  7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
  8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
  9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
 16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep:*
 17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
 18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
 19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
 20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query % Match | Length | DB | ID | Description |
|---|---|---|---|---|---|---|
| 1 | 1299 | 100.0 | 245 | 10 | US-09-873-829-2 | Sequence 2, Appl |
| 2 | 1299 | 100.0 | 245 | 13 | US-10-017-910-2 | Sequence 2, Appl |
| 3 | 1293 | 99.5 | 246 | 14 | US-10-167-182-17 | Sequence 17, Appl |
| 4 | 1293 | 99.5 | 246 | 14 | US-10-460-623-17 | Sequence 17, Appl |
| 5 | 1293 | 99.5 | 249 | 14 | US-10-050-902-221 | Sequence 221, App |
| 6 | 1293 | 99.5 | 249 | 14 | US-10-050-898-221 | Sequence 221, App |
| 7 | 1293 | 99.5 | 249 | 15 | US-10-289-456-82 | Sequence 82, Appl |
| 8 | 1293 | 99.5 | 250 | 14 | US-10-338-785A-1 | Sequence 1, Appl |
| 9 | 1293 | 99.5 | 250 | 16 | US-10-611-363-1 | Sequence 1, Appl |
| 10 | 1293 | 99.5 | 270 | 15 | US-10-289-456-80 | Sequence 80, Appl |
| 11 | 1293 | 99.5 | 317 | 9 | US-09-813-329-7 | Sequence 7, Appli |
| 12 | 1293 | 99.5 | 317 | 9 | US-09-871-956-13 | Sequence 13, Appl |
| 13 | 1293 | 99.5 | 317 | 9 | US-09-957-944-6 | Sequence 6, Appli |
| 14 | 1293 | 99.5 | 317 | 9 | US-09-865-363-13 | Sequence 13, Appl |
| 15 | 1293 | 99.5 | 317 | 9 | US-09-877-650-13 | Sequence 13, Appl |
| 16 | 1293 | 99.5 | 317 | 9 | US-09-871-291-13 | Sequence 13, Appl |
| 17 | 1293 | 99.5 | 317 | 14 | US-10-151-071-10 | Sequence 10, Appl |
| 18 | 1293 | 99.5 | 317 | 14 | US-10-218-547-22 | Sequence 22, Appl |
| 19 | 1293 | 99.5 | 317 | 14 | US-10-405-878-13 | Sequence 13, Appl |
| 20 | 1293 | 99.5 | 317 | 14 | US-10-167-182-11 | Sequence 11, Appl |
| 21 | 1293 | 99.5 | 317 | 14 | US-10-460-623-11 | Sequence 11, Appl |
| 22 | 1293 | 99.5 | 317 | 14 | US-10-289-456-79 | Sequence 79, Appl |
| 23 | 1293 | 99.5 | 317 | 15 | US-10-202-062-22 | Sequence 22, Appl |
| 24 | 1293 | 99.5 | 317 | 15 | US-10-664-801-2 | Sequence 2, Appli |
| 25 | 1293 | 99.5 | 317 | 16 | US-10-381-160-6 | Sequence 6, Appli |
| 26 | 1293 | 99.5 | 317 | 16 | US-10-799-345-12 | Sequence 12, Appl |
| 27 | 1293 | 99.5 | 317 | 17 | US-10-210-951-42 | Sequence 42, Appl |
| 28 | 1288 | 99.2 | 244 | 14 | US-10-050-951-42 | Sequence 42, Appl |
| 29 | 1288 | 99.2 | 244 | 14 | US-10-050-902-222 | Sequence 222, App |
| 30 | 1288 | 99.2 | 244 | 14 | US-10-050-898-222 | Sequence 222, App |
| 31 | 1288 | 99.2 | 244 | 14 | US-10-211-884-42 | Sequence 42, Appl |

## Report 1 (PIR search)

| No. | Score | % | Len | n | ID | Sequence | Description |
|---|---|---|---|---|---|---|---|
| 32 | 1288 | 99.2 | 244 | 14 | US-10-211-858-42 | Sequence 42, Appl | lymphotoxin-beta - |
| 33 | 1288 | 99.2 | 244 | 15 | US-10-289-456-81 | Sequence 81, Appl | tumor necrosis fac |
| 34 | 1108 | 85.3 | 294 | 9 | US-09-871-856-11 | Sequence 11, Appl | tumor necrosis fac |
| 35 | 1108 | 85.3 | 294 | 9 | US-09-865-363-11 | Sequence 11, Appl | tumor necrosis fac |
| 36 | 1108 | 85.3 | 294 | 9 | US-09-871-291-11 | Sequence 11, Appl | tumor necrosis fac |
| 37 | 1108 | 85.3 | 294 | 9 | US-09-877-650-11 | Sequence 11, Appl | tumor necrosis fac |
| 38 | 1108 | 85.3 | 294 | 14 | US-10-405-878-11 | Sequence 11, Appl | tumor necrosis fac |
| 39 | 1108 | 85.3 | 294 | 14 | US-09-957-944-8 | Sequence 8, Appli | tumor necrosis fac |
| 40 | 1108 | 85.3 | 316 | 17 | US-10-799-345-10 | Sequence 10, Appl | tumor necrosis fac |
| 41 | 1101 | 84.8 | 244 | 14 | US-10-167-182-16 | Sequence 16, Appl | tumor necrosis fac |
| 42 | 1101 | 84.8 | 244 | 14 | US-10-460-623-16 | Sequence 16, Appl | lymphotoxin beta - |
| 43 | 1101 | 84.8 | 247 | 14 | US-10-050-902-223 | Sequence 223, App | lymphotoxin beta - |
| 44 | 1101 | 84.8 | 247 | 14 | US-10-289-898-223 | Sequence 223, App | CD40 ligand - mous |
| 45 | 1101 | 84.8 | 247 | 15 | US-10-289-456-85 | Sequence 85, Appl | protein P1 - Entam |

Copyright (c) 1993 - 2004  Compugen Ltd.

GenCore version 5.1.6

Maximum DB seq length: 200000000
Minimum DB seq length: 0

Total number of hits satisfying chosen parameters:      283416

Searched:      283416 seqs, 96216763 residues

Scoring table:  BLOSUM62       Gapop 10.0 ,  Gapext 0.5

Sequence:     1 QMDPNRISEDGTHCIYRLLR..........LLDPDQDATYFGAFKVRDID 245

Perfect score:  1299

Title:          US-10-017-910-2

Run on:         November  1, 2004, 20:51:41 ; Search time 22.2727 Seconds
                (without alignments)
                1058.384 Million cell updates/sec

OM protein - protein search, using sw model

Post-processing:  Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries

Database :   PIR.79:*
             1:  pir1:*
             2:  pir2:*
             3:  pir3:*
             4:  pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

### SUMMARIES

| Result No. | Score | Query Match Length | DB | ID | Description |
|---|---|---|---|---|---|
| 1 | 156 | 12.0 | 261 | 2 | S53090 | CD40 ligand - bovi |
| 2 | 153 | 11.8 | 279 | 2 | A53062 | Fas ligand - mouse |
| 3 | 149 | 11.5 | 261 | 2 | I53476 | CD40 ligand - huma |
| 4 | 146.5 | 11.3 | 281 | 2 | I38707 | Fas ligand - human |
| 5 | 141 | 10.9 | 234 | 1 | JH0529 | tumor necrosis fac |
| 6 | 140 | 10.8 | 278 | 2 | A49266 | fas ligand - rat |
| 7 | 137.5 | 10.6 | 235 | 1 | QWMSN | tumor necrosis fac |
| 8 | 132.5 | 10.2 | 235 | 2 | I54490 | tumor necrosis fac |
| 9 | 130.5 | 10.0 | 234 | 1 | A25451 | tumor necrosis fac |

---

## Report 2 (UniProt search)

| No. | Score | % | Len | DB | ID | Description |
|---|---|---|---|---|---|---|
| 10 | 129.5 | 10.0 | 306 | 2 | I49139 | lymphotoxin-beta - |
| 11 | 129 | 9.9 | 233 | 1 | QWHUN | tumor necrosis fac |
| 12 | 127.5 | 9.8 | 233 | 1 | S24642 | tumor necrosis fac |
| 13 | 127.5 | 9.8 | 235 | 2 | JU0029 | tumor necrosis fac |
| 14 | 126.5 | 9.7 | 185 | 2 | S52715 | tumor necrosis fac |
| 15 | 126 | 9.7 | 232 | 2 | S12606 | tumor necrosis fac |
| 16 | 126 | 9.7 | 233 | 1 | S22052 | tumor necrosis fac |
| 17 | 125 | 9.6 | 193 | 2 | S06192 | tumor necrosis fac |
| 18 | 124 | 9.5 | 234 | 1 | JQ1344 | tumor necrosis fac |
| 19 | 117 | 9.0 | 233 | 1 | S11688 | tumor necrosis fac |
| 20 | 116 | 8.9 | 244 | 2 | A46066 | lymphotoxin beta - |
| 21 | 100.5 | 7.7 | 260 | 2 | S21738 | CD40 ligand - mous |
| 22 | 93 | 7.2 | 639 | 2 | A32935 | protein P1 - Entam |
| 23 | 93 | 7.2 | 1114 | 2 | JH0284 | 125K surface antig |
| 24 | 90.5 | 7.0 | 205 | 1 | QWHUX | lymphotoxin alpha |
| 25 | 88.5 | 6.8 | 450 | 1 | S38114 | hypothetical prote |
| 26 | 88 | 6.8 | 160 | 2 | T17005 | major allergen Mal |
| 27 | 88 | 6.8 | 202 | 1 | B27303 | tumor necrosis fac |
| 28 | 87.5 | 6.7 | 367 | 2 | AE1180 | tumor necrosis fac |
| 29 | 87.5 | 6.7 | 565 | 2 | C89893 | B. subtilis YxjH a |
| 30 | 87.5 | 6.7 | 578 | 2 | S51379 | hypothetical prote |
| 31 | 87 | 6.7 | 794 | 2 | S73328 | probable phosphoes |
| 32 | 86.5 | 6.7 | 640 | 2 | B32935 | probable lipoprote |
| 33 | 86.5 | 6.7 | 1302 | 2 | C81182 | hypothetical prote |
| 34 | 86.5 | 6.7 | 1829 | 2 | S35027 | iron-regulated pro |
| 35 | 86.5 | 6.6 | 160 | 2 | B81086 | cytotoxin RTX homo |
| 36 | 85.5 | 6.5 | 471 | 2 | T17006 | iron-regulated pro |
| 37 | 85 | 6.5 | 486 | 2 | C64765 | yaiT protein precu |
| 38 | 85 | 6.5 | 746 | 2 | PS0154 | major allergen Mal |
| 39 | 84.5 | 6.5 | 397 | 2 | G84461 | 125K surface antig |
| 40 | 84 | 6.5 | 1151 | 2 | S03722 | hypothetical prote |
| 41 | 84 | 6.4 | 197 | 1 | JH0309 | DNA-directed DNA p |
| 42 | 83.5 | 6.4 | 197 | 1 | A26916 | tumor necrosis fac |
| 43 | 83.5 | 6.4 | 399 | 2 | T15566 | ribonucleoside-dip |
| 44 | 83.5 | 6.4 | 2325 | 2 |  | hypothetical prote |
| 45 | 83 | 6.4 | 202 | 1 | JN0869 | tumor necrosis fac |

Copyright (c) 1993 - 2004  Compugen Ltd.

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on:         November  1, 2004, 20:43:45 ; Search time 111.8 Seconds
                (without alignments)
                1260.880 Million cell updates/sec

Title:          US-10-017-910-2

Perfect score:  1299

Sequence:     1 QMDPNRISEDGTHCIYRLLR..........LLDPDQDATYFGAFKVRDID 245

Scoring table:  BLOSUM62       Gapop 10.0 ,  Gapext 0.5

Searched:      1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters:      1825181

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing:  Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries

Database :   UniProt_02:*
             1:  uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query Match | Length | DB | ID | Description |
|---|---|---|---|---|---|---|
| 1 | 1293 | 99.5 | 317 | 1 | TN11_HUMAN | O14788 h tumor nec |
| 2 | 1288 | 99.2 | 244 | 1 | BAB79693 | Bab79693 homo sapi |
| 3 | 1101 | 84.8 | 316 | 1 | TN11_MOUSE | O35235 m tumor nec |
| 4 | 1092 | 84.1 | 318 | 1 | TN11_RAT | Q9ese2 r tumor nec |
| 5 | 249.5 | 19.2 | 317 | 2 | Q72YX9 | Q72yx9 brachydanio |
| 6 | 241 | 18.6 | 304 | 2 | Q71F2 | Q71f2 gallus gall |
| 7 | 236.5 | 18.2 | 214 | 2 | Q9DZ5 | Q9dz5 brachydanio |
| 8 | 234.5 | 18.1 | 281 | 1 | TN10_HUMAN | P50591 homo sapien |
| 9 | 234 | 18.1 | 281 | 2 | CAG33176 | Cag33176 homo sapi |
| 10 | 234 | 18.0 | 291 | 1 | TN10_MOUSE | P50592 mus musculu |
| 11 | 233 | 17.9 | 299 | 2 | Q6DHG9 | Q6dhg9 brachydanio |
| 12 | 215.5 | 16.6 | 287 | 2 | Q90WT9 | Q90wt9 gallus gall |
| 13 | 206 | 15.9 | 287 | 2 | Q8K3G0 | Q8k3g0 rattus norv |
| 14 | 180.5 | 13.9 | 252 | 2 | Q8K3Y8 | Q8k3y8 mus musculu |
| 15 | 177 | 13.6 | 95 | 2 | Q6UWL7 | Q6uwl7 homo sapien |
| 16 | 177 | 13.6 | 95 | 2 | Q6UYL3 | Q6uyl3 homo sapien |
| 17 | 177 | 13.6 | 95 | 2 | AAQ88490 | Aaq88490 homo sapi |
| 18 | 177 | 13.6 | 95 | 1 | AAQ89101 | Aaq89101 homo sapi |
| 19 | 175.5 | 13.5 | 252 | 2 | Q80YZ0 | Q80yz0 mus musculu |
| 20 | 173.5 | 13.4 | 252 | 2 | Q8K3Y7 | Q8k3y7 rattus norv |
| 21 | 156 | 12.0 | 261 | 2 | TNF5_BOVIN | P51749 bos taurus |
| 22 | 156 | 12.0 | 279 | 2 | Q7TMV9 | Q7tmv9 mus musculu |
| 23 | 153.5 | 11.8 | 282 | 1 | TNF6_PIG | Q9bea8 sus scrofa |
| 24 | 153 | 11.8 | 279 | 1 | TNF6_MOUSE | P41047 mus musculu |
| 25 | 153 | 11.8 | 279 | 2 | BAC30520 | Bac30520 mus muscu |
| 26 | 152.5 | 11.7 | 251 | 2 | Q8NFE9 | Q8nfe9 homo sapien |
| 27 | 152.5 | 11.7 | 251 | 2 | AAH69435 | Aah69435 homo sapi |
| 28 | 151 | 11.6 | 280 | 2 | Q861W5 | Q861w5 felis silve |
| 29 | 149 | 11.5 | 261 | 1 | TNF5_AOTTR | Q9bdm3 aotus trivi |
| 30 | 149 | 11.5 | 261 | 1 | TNF5_CALJA | Q9bdn3 callithrix |
| 31 | 149 | 11.5 | 261 | 1 | TNF5_HUMAN | P29965 homo sapien |
| 32 | 149 | 11.5 | 261 | 2 | AAH71754 | Aah71754 homo sapi |
| 33 | 148 | 11.4 | 261 | 2 | TNF5_MACMU | Q9bdc7 macaca mula |
| 34 | 146.5 | 11.3 | 280 | 1 | TNF6_MACMU | Q9myl6 macaca mula |
| 35 | 146.5 | 11.3 | 281 | 2 | TNF6_HUMAN | P48023 homo sapien |
| 36 | 146.5 | 11.3 | 281 | 2 | AAO43991 | Aao43991 homo sapi |
| 37 | 144.5 | 11.1 | 280 | 2 | TNF6_CERTO | Q9bdn1 cercocebus |
| 38 | 142 | 10.9 | 234 | 1 | TNFA_CAVPO | P51435 cavia porce |
| 39 | 142 | 10.9 | 272 | 1 | TNF5_CHICK | Q9i8d8 gallus gall |
| 40 | 141.5 | 10.9 | 239 | 1 | TN14_MOUSE | Q9qyh9 mus musculu |
| 41 | 141 | 10.9 | 174 | 1 | TN15_HUMAN | O95150 homo sapien |
| 42 | 141 | 10.9 | 234 | 1 | TNFA_SHEEP | P23383 ovis aries |
| 43 | 140 | 10.7 | 278 | 1 | TNF6_RAT | P36940 rattus norv |
| 44 | 139 | 10.7 | 234 | 1 | TNFA_CAPHI | P13296 capra hircu |
| 45 | 137.5 | 10.6 | 235 | 1 | TNFA_MOUSE | P06804 mus musculu |

OM protein - protein search, using sw model

Run on:  November 1, 2004, 20:43:02 ; Search time 127,301 Seconds
(without alignments)
890.474 Million cell updates/sec

---

Title: US-10-017-910-4
Perfect score: 1675
Sequence: 1 MRRASRDYGKYLRSSEEMGS............LLDPDQDATYFGAFKYQDID 316

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Database :
1: A_Geneseq_23Sep04:*
2: geneseqp19808:*
3: geneseqp19990s:*
4: geneseqp20000s:*
5: geneseqp20001s:*
6: geneseqp20028:*
7: geneseqp20003as:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query Match | Length | DB | ID | Description |
|---|---|---|---|---|---|---|
| 1 | 1675 | 100.0 | 316 | 2 | AAW83017 | Aaw83017 Osteoclas |
| 2 | 1675 | 100.0 | 316 | 2 | AAW83194 | Aaw83194 Human ost |
| 3 | 1675 | 100.0 | 316 | 2 | AAW59654 | Aaw59654 Amino aci |
| 4 | 1675 | 100.0 | 316 | 2 | AAY17874 | Aay17874 Murine TR |
| 5 | 1675 | 100.0 | 316 | 3 | AAY91024 | Aay91024 Mouse OBM |
| 6 | 1675 | 100.0 | 316 | 3 | AAY84418 | Aay84418 Amino aci |
| 7 | 1675 | 100.0 | 316 | 3 | AAY84419 | Aay84419 Amino aci |
| 8 | 1675 | 100.0 | 316 | 5 | AAU78289 | Aau78289 Mouse TRA |
| 9 | 1675 | 100.0 | 316 | 6 | ABR42071 | Abr42071 Human RAN |
| 10 | 1675 | 100.0 | 316 | 6 | ABB99477 | Abb99477 Amino aci |
| 11 | 1675 | 100.0 | 316 | 6 | ABU08463 | Abu08463 Amino aci |
| 12 | 1675 | 100.0 | 316 | 6 | ABR55560 | Abr55560 Amino aci |
| 13 | 1597 | 95.3 | 318 | 4 | ABS55560 | Abs55560 Amino aci |
| 14 | 1554 | 92.8 | 294 | 2 | AAW69956 | Aaw69956 NF-kB rec |
| 15 | 1554 | 92.8 | 294 | 2 | AAW68292 | Aaw68292 NF-kB rec |
| 16 | 1554 | 92.8 | 294 | 2 | AAE08737 | Aae08737 Murine re |
| 17 | 1554 | 92.8 | 294 | 2 | AAE04425 | Aae04425 Murine re |
| 18 | 1554 | 92.8 | 294 | 4 | AAE01992 | Aae01992 Murine RA |
| 19 | 1554 | 92.8 | 294 | 5 | AAB26102 | Aab26102 Mouse RAN |
| 20 | 1554 | 92.8 | 294 | 7 | ADB16986 | Adb16986 Murine re |
| 21 | 1554 | 92.8 | 294 | 7 | ADC73000 | Adc73000 Murine RA |
| 22 | 1554 | 92.8 | 294 | 7 | ADC78266 | Adc78266 Murine RA |
| 23 | 1554 | 92.8 | 294 | 7 | ADG46721 | Adg46721 Murine RA |
| 24 | 1417.5 | 84.6 | 317 | 2 | AAW83195 | Aaw83195 Human ost |
| 25 | 1417.5 | 84.6 | 317 | 2 | AAW69957 | Aaw69957 Human ost |
| 26 | 1417.5 | 84.6 | 317 | 2 | AAW68293 | Aaw68293 NF-kB rec |
| 27 | 1417.5 | 84.6 | 317 | 2 | AAE08738 | Aae08738 Human rec |
| 28 | 1417.5 | 84.6 | 317 | 3 | AAY84417 | Aay84417 Amino aci |
| 29 | 1417.5 | 84.6 | 317 | 3 | AAE04426 | Aae04426 Human rec |
| 30 | 1417.5 | 84.6 | 317 | 4 | AAE01993 | Aae01993 Human ful |

## OM protein – protein search, using sw model

```
                        GenCore version 5.1.6
                  Copyright (c) 1993 - 2004 Compugen Ltd.
```

| | |
|---|---|
| Run on: | November 1, 2004, 20:51:51 ; Search time 31.5437 Seconds |
| | (without alignments) |
| | 664.364 Million cell updates/sec |

```
Title:          US-10-017-910-4
Perfect score:  1675
Sequence:       1 MRASRDYGKYLRSSEEMGS...........LLDPDQDATYFGAFKVQDID 316

Scoring table:  BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched:       478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters:   478139

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries
```

| No. | Score | % | Len | DB | ID | Description |
|---|---|---|---|---|---|---|
| 31 | 1417.5 | 84.6 | 317 | 5 | Abb08134 | Human RAN |
| 32 | 1417.5 | 84.6 | 317 | 5 | Aae26103 | Human RAN |
| 33 | 1417.5 | 84.6 | 317 | 5 | Abg31631 | Human RAN |
| 34 | 1417.5 | 84.6 | 317 | 5 | Aau78285 | Human TRA |
| 35 | 1417.5 | 84.6 | 317 | 5 | Aao19096 | C neoform |
| 36 | 1417.5 | 84.6 | 317 | 6 | Abp55108 | Human ost |
| 37 | 1417.5 | 84.6 | 317 | 6 | Aae34364 | Human rec |
| 38 | 1417.5 | 84.6 | 317 | 6 | Abr42314 | Human RAN |
| 39 | 1417.5 | 84.6 | 317 | 6 | Adb16988 | Human rec |
| 40 | 1417.5 | 84.6 | 317 | 7 | Adc35204 | Human TNF |
| 41 | 1417.5 | 84.6 | 317 | 7 | Adc73002 | Human RAN |
| 42 | 1417.5 | 84.6 | 317 | 7 | Adc78268 | Human RAN |
| 43 | 1417.5 | 84.6 | 317 | 7 | Abw02277 | Human RAN |
| 44 | 1417.5 | 84.6 | 317 | 7 | Adg46723 | Human RAN |
| 45 | 1417.5 | 84.6 | 317 | 7 | Adj82112 | Protein f |

```
Databases :     Issued_Patents_AA:*
                1: /cgn2_6/ptdata/1/iaa/5A_COMB.pep:*
                2: /cgn2_6/ptdata/1/iaa/5B_COMB.pep:*
                3: /cgn2_6/ptdata/1/iaa/6A_COMB.pep:*
                4: /cgn2_6/ptdata/1/iaa/6B_COMB.pep:*
                5: /cgn2_6/ptdata/1/iaa/PCTUS_COMB.pep:*
                6: /cgn2_6/ptdata/1/iaa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
```

### SUMMARIES

| Result No. | Score | % Match | Query Length | DB | ID | Description |
|---|---|---|---|---|---|---|
| 1 | 1675 | 100.0 | 316 | 2 | US-08-842-842-7 | Sequence 7, Appli |
| 2 | 1675 | 100.0 | 316 | 3 | US-08-989-362-2 | Sequence 2, Appli |
| 3 | 1675 | 100.0 | 316 | 3 | US-08-052-521C-2 | Sequence 2, Appli |
| 4 | 1675 | 100.0 | 316 | 4 | US-09-671-658A-2 | Sequence 2, Appli |
| 5 | 1675 | 100.0 | 316 | 4 | US-09-396-937-4 | Sequence 4, Appli |
| 6 | 1675 | 100.0 | 316 | 4 | US-09-396-937-6 | Sequence 6, Appli |

---

## OM protein – protein search, using sw model

```
                        GenCore version 5.1.6
                  Copyright (c) 1993 - 2004 Compugen Ltd.
```

| | |
|---|---|
| Run on: | November 1, 2004, 20:54:17 ; Search time 95.1943 Seconds |
| | (without alignments) |
| | 1076.243 Million cell updates/sec |

```
Title:          US-10-017-910-4
Perfect score:  1675
Sequence:       1 MRASRDYGKYLRSSEEMGS...........LLDPDQDATYFGAFKVQDID 316

Scoring table:  BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched:       1370721 seqs, 324215800 residues

Total number of hits satisfying chosen parameters:   1370721

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries
```

| No. | Score | % | Len | DB | ID | Description |
|---|---|---|---|---|---|---|
| 7 | 1554 | 92.8 | 294 | 3 | US-08-996-139-11 | Sequence 11, Appl |
| 8 | 1554 | 92.8 | 294 | 3 | US-08-995-659-11 | Sequence 11, Appl |
| 9 | 1554 | 92.8 | 294 | 3 | US-09-215-649A-11 | Sequence 11, Appl |
| 10 | 1554 | 92.8 | 294 | 4 | US-09-577-780-11 | Sequence 11, Appl |
| 11 | 1554 | 92.8 | 294 | 4 | US-09-577-800-11 | Sequence 11, Appl |
| 12 | 1554 | 92.8 | 294 | 4 | US-09-577-496-11 | Sequence 11, Appl |
| 13 | 1554 | 92.8 | 294 | 4 | US-09-466-496-11 | Sequence 11, Appl |
| 14 | 1554 | 92.8 | 294 | 4 | US-09-871-856-11 | Sequence 11, Appl |
| 15 | 1554 | 92.8 | 294 | 4 | US-09-871-291-11 | Sequence 11, Appl |
| 16 | 1554 | 92.8 | 294 | 4 | US-09-865-363-11 | Sequence 11, Appl |
| 17 | 1554 | 92.8 | 294 | 3 | US-09-396-937-2 | Sequence 2, Appl |
| 18 | 1417.5 | 84.6 | 317 | 3 | US-09-877-650-13 | Sequence 13, Appl |
| 19 | 1417.5 | 84.6 | 317 | 3 | US-09-215-649A-13 | Sequence 13, Appl |
| 20 | 1417.5 | 84.6 | 317 | 3 | US-08-995-659-13 | Sequence 4, Appl |
| 21 | 1417.5 | 84.6 | 317 | 3 | US-09-052-521C-4 | Sequence 13, Appl |
| 22 | 1417.5 | 84.6 | 317 | 4 | US-09-577-780-13 | Sequence 13, Appl |
| 23 | 1417.5 | 84.6 | 317 | 4 | US-09-577-800-13 | Sequence 13, Appl |
| 24 | 1417.5 | 84.6 | 317 | 4 | US-09-466-496-13 | Sequence 13, Appl |
| 25 | 1417.5 | 84.6 | 317 | 4 | US-09-871-856-13 | Sequence 13, Appl |
| 26 | 1417.5 | 84.6 | 317 | 4 | US-09-871-291-13 | Sequence 13, Appl |
| 27 | 1417.5 | 84.6 | 317 | 4 | US-09-865-363-13 | Sequence 2, Appl |
| 28 | 1417.5 | 84.6 | 317 | 4 | US-09-396-937-13 | Sequence 13, Appl |
| 29 | 852 | 50.9 | 173 | 4 | US-09-877-650-13 | Sequence 8, Appl |
| 30 | 852 | 50.9 | 187 | 4 | US-09-396-937-10 | Sequence 10, Appl |
| 31 | 842 | 50.3 | 188 | 4 | US-09-396-937-8 | Sequence 12, Appl |
| 32 | 804.5 | 48.0 | 173 | 4 | US-09-396-937-12 | Sequence 14, Appl |
| 33 | 794.5 | 47.4 | 182 | 4 | US-09-396-937-14 | Sequence 16, Appl |
| 34 | 771 | 46.0 | 173 | 4 | US-09-396-937-16 | Sequence 18, Appl |
| 35 | 732 | 43.7 | 173 | 4 | US-09-396-937-18 | Sequence 20, Appl |
| 36 | 422 | 25.2 | 77 | 4 | US-09-396-937-20 | Sequence 16, Appl |
| 37 | 363 | 21.7 | 77 | 4 | US-09-632-287A-20 | Sequence 3, Appl |
| 38 | 258.5 | 15.4 | 279 | 3 | US-09-632-287A-10 | Sequence 11, Appl |
| 39 | 258.5 | 15.4 | 281 | 1 | US-09-072-993C-3 | Sequence 3, Appl |
| 40 | 258.5 | 15.4 | 281 | 3 | US-08-670-354-2 | Sequence 1, Appl |
| 41 | 258.5 | 15.4 | 281 | 3 | US-08-584-031-1 | Sequence 1, Appl |
| 42 | 258.5 | 15.4 | 281 | 3 | US-08-780-496-1 | Sequence 10, Appl |
| 43 | 258.5 | 15.4 | 281 | 3 | US-08-883-086-10 | Sequence 2, Appl |
| 44 | 258.5 | 15.4 | 281 | 3 | US-09-320-424-2 | Sequence 6, Appl |
| 45 | 258.5 | 15.4 | 281 | 4 | US-09-333-593A-6 | Sequence 11, Appl |
| | | | | | US-09-157-864-11 | |

**Databases :**

Published_Applications_AA:*
1: /cgn2_6/ptcdata/2/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptcdata/2/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptcdata/2/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptcdata/2/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptcdata/2/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptcdata/2/pubpaa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/ptcdata/2/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptcdata/2/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptcdata/2/pubpaa/US09A_PUBCOMB.pep:*
10: /cgn2_6/ptcdata/2/pubpaa/US09B_PUBCOMB.pep:*
11: /cgn2_6/ptcdata/2/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptcdata/2/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptcdata/2/pubpaa/US10A_PUBCOMB.pep:*
14: /cgn2_6/ptcdata/2/pubpaa/US10B_PUBCOMB.pep:*
15: /cgn2_6/ptcdata/2/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptcdata/2/pubpaa/US10D_PUBCOMB.pep:*
17: /cgn2_6/ptcdata/2/pubpaa/US10_NEW_PUB.pep:*
18: /cgn2_6/ptcdata/2/pubpaa/US11_NEW_PUB.pep:*
19: /cgn2_6/ptcdata/2/pubpaa/US60_NEW_PUB.pep:*
20: /cgn2_6/ptcdata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query Match | Length | DB | ID | Description |
|---|---|---|---|---|---|---|
| 1 | 1675 | 100.0 | 316 | 10 | US-09-079-569-7 | Sequence 7, Appli |
| 2 | 1675 | 100.0 | 316 | 10 | US-09-873-829-4 | Sequence 4, Appli |
| 3 | 1675 | 100.0 | 316 | 13 | US-10-017-910-4 | Sequence 4, Appli |
| 4 | 1675 | 100.0 | 316 | 14 | US-10-105-057-2 | Sequence 2, Appli |
| 5 | 1675 | 100.0 | 316 | 14 | US-10-272-411-19 | Sequence 19, Appl |
| 6 | 1675 | 100.0 | 316 | 14 | US-10-272-328A-19 | Sequence 19, Appl |
| 7 | 1675 | 100.0 | 316 | 14 | US-10-326-052-2 | Sequence 2, Appli |
| 8 | 1675 | 100.0 | 316 | 14 | US-10-167-182-1 | Sequence 1, Appli |
| 9 | 1675 | 100.0 | 316 | 14 | US-10-460-623-1 | Sequence 1, Appli |
| 10 | 1675 | 100.0 | 316 | 16 | US-10-664-801-4 | Sequence 4, Appli |
| 11 | 1675 | 100.0 | 316 | 16 | US-10-664-801-6 | Sequence 6, Appli |
| 12 | 1668 | 99.6 | 316 | 9 | US-10-957-944-8 | Sequence 8, Appli |
| 13 | 1668 | 99.6 | 316 | 17 | US-10-799-345-10 | Sequence 10, Appl |
| 14 | 1554 | 92.8 | 294 | 9 | US-09-871-856-11 | Sequence 11, Appl |
| 15 | 1554 | 92.8 | 294 | 9 | US-09-865-363-11 | Sequence 11, Appl |
| 16 | 1554 | 92.8 | 294 | 9 | US-09-871-291-11 | Sequence 11, Appl |
| 17 | 1554 | 92.8 | 294 | 14 | US-09-877-650-11 | Sequence 11, Appl |
| 18 | 1554 | 92.8 | 294 | 14 | US-10-405-878-11 | Sequence 11, Appl |
| 19 | 1417.5 | 84.6 | 317 | 14 | US-09-813-329-7 | Sequence 7, Appli |
| 20 | 1417.5 | 84.6 | 317 | 9 | US-09-871-856-13 | Sequence 13, Appl |
| 21 | 1417.5 | 84.6 | 317 | 9 | US-09-957-944-6 | Sequence 6, Appli |
| 22 | 1417.5 | 84.6 | 317 | 9 | US-09-865-363-13 | Sequence 13, Appl |
| 23 | 1417.5 | 84.6 | 317 | 9 | US-09-871-291-13 | Sequence 13, Appl |
| 24 | 1417.5 | 84.6 | 317 | 9 | US-09-877-650-13 | Sequence 13, Appl |
| 25 | 1417.5 | 84.6 | 317 | 14 | US-10-151-071-10 | Sequence 10, Appl |
| 26 | 1417.5 | 84.6 | 317 | 14 | US-10-218-547-22 | Sequence 22, Appl |
| 27 | 1417.5 | 84.6 | 317 | 14 | US-10-405-878-13 | Sequence 13, Appl |
| 28 | 1417.5 | 84.6 | 317 | 14 | US-10-167-182-11 | Sequence 11, Appl |
| 29 | 1417.5 | 84.6 | 317 | 14 | US-10-310-793-28 | Sequence 28, Appl |
| 30 | 1417.5 | 84.6 | 317 | 14 | US-10-460-623-11 | Sequence 11, Appl |
| 31 | 1417.5 | 84.6 | 317 | 15 | US-10-289-456-79 | Sequence 79, Appl |
| 32 | 1417.5 | 84.6 | 317 | 15 | US-10-202-062-22 | Sequence 22, Appl |
| 33 | 1417.5 | 84.6 | 317 | 16 | US-10-664-801-2 | Sequence 2, Appli |
| 34 | 1417.5 | 84.6 | 317 | 16 | US-10-381-160-6 | Sequence 6, Appli |
| 35 | 1417.5 | 84.6 | 317 | 17 | US-10-799-345-12 | Sequence 12, Appl |
| 36 | 1325 | 79.1 | 249 | 14 | US-10-338-785A-3 | Sequence 3, Appli |
| 37 | 1325 | 79.1 | 249 | 16 | US-10-611-363-3 | Sequence 3, Appli |
| 38 | 1315 | 78.5 | 247 | 14 | US-10-050-902-223 | Sequence 223, App |
| 39 | 1315 | 78.5 | 247 | 14 | US-10-050-898-223 | Sequence 223, App |
| 40 | 1315 | 78.5 | 247 | 15 | US-10-289-456-85 | Sequence 85, Appl |
| 41 | 1297 | 77.4 | 244 | 14 | US-10-167-182-16 | Sequence 16, Appl |
| 42 | 1297 | 77.4 | 244 | 14 | US-10-460-623-16 | Sequence 16, Appl |
| 43 | 1220 | 72.8 | 270 | 15 | US-10-289-456-80 | Sequence 80, Appl |
| 44 | 1127 | 67.3 | 249 | 14 | US-10-050-902-221 | Sequence 221, App |
| 45 | 1127 | 67.3 | 249 | 14 | US-10-050-898-221 | Sequence 221, App |

OM protein - protein search, using sw model

Run on: November 1, 2004, 20:51:41 ; Search time 28.7273 Seconds
(without alignments)
1058.384 Million cell updates/sec

Title: US-10-017-910-4
Perfect score: 1675
Sequence: 1 MRRASRDYGKYLRSSEEMGS.........LLDPDQDATYFGAFKVQDID 316

Searched: 283416 seqs, 96216763 residues

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: PIR_79:*
2: pir1:*
3: pir2:*
4: pir3:*
pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query Match | Length | DB | ID | Description |
|---|---|---|---|---|---|---|
| 1 | 185.5 | 11.1 | 261 | 2 | S53090 | CD40 ligand - bovi |
| 2 | 183 | 10.9 | 278 | 2 | A49266 | fas ligand - rat |
| 3 | 182 | 10.9 | 279 | 2 | A53062 | Fas ligand - mouse |
| 4 | 173.5 | 10.4 | 281 | 2 | I38707 | Fas ligand - human |
| 5 | 171.5 | 10.2 | 261 | 2 | I53476 | CD40 ligand - huma |
| 6 | 157 | 9.4 | 260 | 2 | S21738 | CD40 ligand - mous |
| 7 | 149 | 8.9 | 234 | 1 | JQ1344 | tumor necrosis fac |
| 8 | 146.5 | 8.7 | 235 | 1 | QWMSN | tumor necrosis fac |
| 9 | 143.5 | 8.6 | 233 | 1 | S22052 | tumor necrosis fac |
| 10 | 141 | 8.4 | 234 | 1 | JH0529 | tumor necrosis fac |
| 11 | 140 | 8.4 | 233 | 1 | S11688 | tumor necrosis fac |
| 12 | 139.5 | 8.3 | 233 | 1 | QWHUN | tumor necrosis fac |
| 13 | 137.5 | 8.2 | 234 | 1 | A25451 | tumor necrosis fac |
| 14 | 135.5 | 8.1 | 235 | 2 | I54490 | tumor necrosis fac |

OM protein - protein search, using sw model

Copyright (c) 1993 - 2004 Compugen Ltd.

GenCore version 5.1.6

Run on: November 1, 2004, 20:43:45 ; Search time 144.2 Seconds
(without alignments)
1260.880 Million cell updates/sec

Title: US-10-017-910-4
Perfect score: 1675
Sequence: 1 MRRASRDYGKYLRSSEEMGS.........LLDFDQDATYFGAFKVQDID 316

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Database : UniProt_02:*
  1: uniprot_sprot:*
  2: uniprot_trembl:*

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
  Maximum Match 100%
  Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | % Query Match | Length | DB | ID | Description |
|---|---|---|---|---|---|---|
| 1 | 1675 | 100.0 | 316 | 1 | TN11_MOUSE | 035235 m tumor nec |
| 2 | 1597 | 95.3 | 318 | 1 | TN11_RAT | Q9ese2 r tumor nec |
| 3 | 1417.5 | 84.6 | 317 | 1 | TN11_HUMAN | O14788 h tumor nec |
| 4 | 1100 | 65.7 | 244 | 2 | BAB79693 | Bab79693 homo sapi |
| 5 | 283 | 16.9 | 317 | 2 | Q7ZX9 | Q7zyx9 brachydanio |
| 6 | 263.5 | 15.7 | 214 | 2 | Q9DD25 | Q9dd25 brachydanio |
| 7 | 261 | 15.6 | 304 | 2 | Q7TIF2 | Q7tif2 gallus gall |
| 8 | 258.5 | 15.4 | 281 | 1 | TN10_HUMAN | P50591 homo sapien |
| 9 | 258 | 15.4 | 281 | 2 | CAG33176 | Cag33176 homo sapi |
| 10 | 250 | 14.9 | 299 | 2 | Q6DHG9 | Q6dhg9 brachydanio |
| 11 | 244 | 14.6 | 291 | 1 | TN10_MOUSE | P50592 mus musculu |
| 12 | 221.5 | 13.2 | 287 | 2 | Q8K3G0 | Q8k3g0 rattus norv |
| 13 | 217.5 | 13.0 | 287 | 2 | Q90WT9 | Q90wt9 gallus gall |
| 14 | 188.5 | 11.3 | 261 | 1 | TNF5_CALJA | Q9bdn3 callithrix |
| 15 | 185.5 | 11.1 | 252 | 2 | Q8K3Y8 | Q8k3y8 mus musculu |
| 16 | 185 | 11.1 | 261 | 1 | TNF5_BOVIN | P51749 bos taurus |
| 17 | 183 | 11.0 | 279 | 2 | Q7TWV9 | Q7twv9 mus musculu |
| 18 | 182.5 | 10.9 | 278 | 1 | TNF6_RAT | P36940 rattus norv |
| 19 | 182 | 10.9 | 261 | 1 | TNF6_AOTTR | Q9bdm3 aotus trivi |
| 20 | 182 | 10.9 | 279 | 1 | TNF6_MOUSE | P41047 mus musculu |
| 21 | 180.5 | 10.9 | 279 | 2 | BAC30520 | Bac30520 mus muscu |
| 22 | 179.5 | 10.8 | 252 | 2 | Q80YZ0 | Q80yz0 mus musculu |
| 23 | 179.5 | 10.7 | 282 | 1 | TNF6_PIG | Q9bea8 sus scrofa |
| 24 | 178.5 | 10.7 | 280 | 2 | Q861W5 | Q861w5 felis silve |
| 25 | 178 | 10.7 | 280 | 2 | Q9MYL6 | Q9myl6 macaca mula |
| 26 | 177 | 10.6 | 280 | 2 | Q9BDH1 | Q9bdh1 cercocebus |
| 27 | 176.5 | 10.6 | 261 | 2 | TNF6_MACMU | Q9bdc7 macaca mula |
| 28 | 176.5 | 10.5 | 261 | 2 | TNF6_CERTO | Q6uwl7 macaca mula |
| 29 | 176 | 10.5 | 95 | 2 | Q6UWL7 | Q6uwl7 homo sapien |
| 30 | 176 | 10.5 | 95 | 2 | Q6UY13 | Q6uy13 homo sapien |
| 31 | 176 | 10.5 | 95 | 2 | AAQ88490 | Aaq88490 homo sapi |
| 32 | 175.5 | 10.5 | 252 | 2 | AAQ89101 | Aaq89101 homo sapi |
| 33 | 173.5 | 10.4 | 281 | 2 | Q8K3Y7 | Q8k3y7 rattus norv |
| 34 | 173.5 | 10.4 | 281 | 2 | TNF6_HUMAN | Aao43991 homo sapi |
| 35 | 171.5 | 10.2 | 261 | 2 | AAO43991 | P48023 homo sapien |
| 36 | 171.5 | 10.2 | 261 | 1 | P29965 | P29965 homo sapien |
| 37 | 167.5 | 10.0 | 272 | 2 | AAH71754 | Aah71754 homo sapi |
| 38 | 164 | 9.8 | 260 | 1 | TNF5_CHICK | Q9i8d8 gallus gall |
| 39 | 159.5 | 9.5 | 261 | 2 | TNF5_PIG | O97605 felis silve |
| 40 | 158.5 | 9.5 | 251 | 1 | TNF5_FELCA | Q95mg5 sus scrofa |
| 41 | 158.5 | 9.5 | 251 | 2 | Q8NFE9 | Q8nfe9 homo sapien |
| 42 | 157 | 9.4 | 234 | 1 | AAH69435 | Aah69435 homo sapi |
| 43 | 157 | 9.4 | 260 | 1 | TNFA_CAVPO | P51435 cavia porce |
| 44 | 154 | 9.5 | 260 | 1 | TNF5_MOUSE | P27548 mus musculu |
| 45 | 154 | 9.2 | 260 | 1 | TNF5_CANFA | O97626 canis famil |

An additional set of lower-scoring hits is listed with the following Score / % Query Match / Length / DB / ID / Description values:

| Score | % Query Match | Length | DB | ID | Description |
|---|---|---|---|---|---|
| 133.5 | 8.0 | 233 | 1 | S24642 | tumor necrosis fac |
| 133 | 7.9 | 185 | 2 | S52715 | tumor necrosis fac |
| 133 | 7.9 | 232 | 1 | S12606 | tumor necrosis fac |
| 129.5 | 7.7 | 235 | 2 | JU0029 | tumor necrosis fac |
| 129.5 | 7.7 | 306 | 2 | 149139 | lymphotoxin-beta - |
| 117 | 7.0 | 244 | 2 | A46066 | lymphotoxin beta - |
| 115.5 | 6.9 | 193 | 2 | S06192 | tumor necrosis fac |
| 103.5 | 6.2 | 340 | 2 | S49742 | hypothetical prote |
| 103 | 6.1 | 3848 | 2 | T17414 | Tlpc protein - sli |
| 99.5 | 5.9 | 558 | 2 | T23649 | hypothetical prote |
| 99 | 5.9 | 440 | 2 | I49681 | glyceraldehyde-3-p |
| 97 | 5.8 | 450 | 2 | S38114 | hypothetical prote |
| 95.5 | 5.7 | 553 | 2 | B55514 | dihydrolipoamide S |
| 94 | 5.6 | 1486 | 2 | B40333 | collagen alpha 1(I |
| 93.5 | 5.6 | 205 | 1 | QWHUX | lymphotoxin alpha |
| 92.5 | 5.5 | 197 | 1 | JH0309 | lymphotoxin alpha |
| 92 | 5.5 | 549 | 2 | JC5926 | secreted klotho pr |
| 92 | 5.5 | 785 | 2 | T23456 | hypothetical prote |
| 92 | 5.5 | 1012 | 2 | JC5925 | membrane klotho pr |
| 90.5 | 5.4 | 658 | 2 | T39500 | serine/threonine-s |
| 90.5 | 5.4 | 750 | 2 | E84475 | probable Athila re |
| 90.5 | 5.4 | 952 | 2 | AC0447 | probable insectici |
| 90 | 5.4 | 3011 | 1 | S40770 | genome polyprotein |
| 89 | 5.3 | 1694 | 2 | S50065 | sialoadhesin - mou |
| 89 | 5.3 | 202 | 1 | B27303 | tumor necrosis fac |
| 88.5 | 5.3 | 477 | 1 | I38409 | adenylyl cyclase-a |
| 88.5 | 5.3 | 1547 | 2 | JQ0096 | hypothetical 176K |
| 88 | 5.3 | 347 | 2 | H75253 | hypothetical prote |
| 88 | 5.3 | 560 | 1 | JQ1221 | probable 60K inner |
| 88 | 5.3 | 1420 | 2 | T37781 | probable cytoskele |
| 88 | 5.3 | 2774 | 2 | A43359 | microtubule-associ |